

CLAIMS

1. (Currently Amended) An anti-virus agent acting against single stranded RNA (+) viruses, comprising the following components (A) and (B),

 (A) a nucleotide sequence directing the synthesis of the complementary strand of the single stranded virus;

 (B)(b) a nucleotide sequence containing at least a regulatory region operably linked to a structural gene encoding a toxin,

 wherein the nucleotide sequence encoding the toxin is positioned in an antisense direction.
2. (Currently Amended) The anti-virus agent of according to claim 1, wherein component (A) is derived from the 5'-and/or 3'-untranslated regions of a ss(+)RNA virus.
3. (Currently Amended) The anti-virus agent of according to claim 2, wherein the component (A) is derived from the 3' untranslated region of the HCV virus.
4. (Currently Amended) The anti-virus agent of claim 1 according to any of the ~~proceeding~~ claims, wherein the regulatory region comprises the Shine-Dalgarno sequence or the internal ribosomal binding site (IRBS) of the genomic RNA of the poliovirus vaccine strain Sabin 2.
5. (Currently Amended) The anti-virus agent of claim 1 according to any of the ~~proceeding~~ claims, wherein the toxin is selected from the group consisting of ~~comprising~~ diptheria exotoxin, diptheria exotoxin A-subunit, Sigella toxin and Disenteria toxin.

6. (Currently Amended) The anti-virus agent of claim 1 ~~according to any of the preceding claims~~, which comprises a DNA or a RNA vector.

Claims 7 - 8 (Canceled).

9. (New) A method for treating a viral disease, comprising: administering to a patient in need of anti-viral therapy an effective amount of an anti-virus agent acting against single stranded RNA (+) viruses, comprising the following components (A) and (B),
- (A) a nucleotide sequence directing the synthesis of the complementary strand of the single stranded virus;
- (B) a nucleotide sequence containing at least a regulatory region operably linked to a structural gene encoding a toxin,

wherein the nucleotide sequence encoding the toxin is positioned in an antisense direction.

10. (New) The method of claim 9, wherein the disease is caused by a virus selected from the group consisting of hepatitis virus type B, C, D or E, the Dengue virus, unclassified flaviviridae, Rubella virus, Yellow fever virus, Dengue virus, bovine viral diarrhoea virus, swine fever virus, and foot and mouth disease.